

Applicants : Yingru Wu, et al.  
Serial No. : 10/594,785  
Filed : September 17, 2007  
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October 1, 2010 Office Action

**Amendments to the Claims**

Please amend the claims by replacing all prior listings of claims with the listing of claims below pursuant to 37 C.F.R. §1.121:

**Listing of Claims:**

1-116. (Cancelled)

117. (Currently amended) A method of increasing ~~altering~~ fibre initiation and/or elongation in a fibre producing plant comprising genetically manipulating the plant such that the production of a polypeptide comprising consecutive amino acids whose sequence is ~~at least 95% identical~~ to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38 is increased when compared to a wild-type fiber producing plant, ~~wherein the polypeptide is produced in the wild-type fiber producing plant at or around anthesis.~~

118. (Withdrawn-currently amended) A method of reducing ~~altering~~ fibre initiation and/or elongation in a fibre producing plant comprising genetically manipulating the plant such that the production of a polypeptide comprising consecutive amino acids whose sequence is ~~at least 95% identical~~ to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38 is reduced when compared to a wild-type fiber producing plant, ~~wherein the polypeptide is produced in the wild-type fiber producing plant at or around anthesis.~~

119. (Previously presented) The method of claim 117 or 118,

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wherein the polypeptide comprises consecutive amino acids whose sequence is set forth in SEQ ID NO: 12.

120. (Currently amended) The method of claim 117, wherein the genetic manipulation comprises exposing the plant to a vector which comprises a nucleotide sequence encoding a polypeptide comprising consecutive amino acids whose sequence is ~~at least~~ 95% identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38.

121. (Withdrawn) The method of claim 118, wherein the genetic manipulation comprises exposing the plant to an antisense polynucleotide or a catalytic polynucleotide which hybridizes to an mRNA molecule encoding the polypeptide, and/or exposing the plant to a dsRNA molecule that specifically down-regulates levels of an mRNA molecule encoding the polypeptide, such that the level of the polypeptide produced by the plant is reduced.

122. (Withdrawn-currently amended) The method of claim 121, wherein the genetic manipulation is exposing the plant to the dsRNA molecule and the dsRNA molecule is double-stranded over at least 19 basepairs whose sequence corresponds to a consecutive sequence set forth in SEQ ID NO: 38, or to a consecutive sequence which is ~~at least~~ 95% identical to the sequence set forth in SEQ ID NO: 38.

123. (Previously presented) The method of claim 117 or 118, wherein the plant is a species of the Genus *Gossypium*.

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124. (Withdrawn—currently amended) A process of assessing the potential of a fibre producing plant to produce fibre, the process comprising analyzing whether the plant has for a genetic variation in a polynucleotide comprising a whose sequence is at least 95% identical to the nucleotide sequence set forth in SEQ ID NO: 38, wherein the polynucleotide is produced in a wild-type fibre producing plant at or around anthesis, and/or analyzing whether the plant for a genetic variation in is capable of expressing a polypeptide comprising an amino acid sequence which is at least 95% identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38.

125. (Withdrawn) The method of claim 124, wherein the polypeptide comprises consecutive amino acids whose sequence is set forth in SEQ ID NO: 12.

126. (Withdrawn—currently amended) A substantially purified and/or recombinant polypeptide selected from the group consisting of:

i) ~~a polypeptide comprising consecutive amino acids whose sequence is set forth in SEQ ID NO: 12, and~~

ii) ~~a polypeptide comprising consecutive amino acids whose sequence is at least 95% identical to the amino acids sequence set forth in SEQ ID NO: 12.~~

127. (Currently amended) An isolated and/or exogenous polynucleotide comprising a polynucleotide selected from

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the group consisting of:

i) a polynucleotide comprising consecutive nucleotides whose nucleotide sequence is set forth in SEQ ID NO: 38; and

~~ii) a polynucleotide comprising consecutive nucleotides whose sequence is at least 95% identical to the nucleotide sequence set forth in SEQ ID NO: 38,~~

~~iii) a polynucleotide which encodes a polypeptide comprising consecutive amino acids whose sequence is at least 95% identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38, and~~

~~iv) a polynucleotide which hybridizes to any one of i) to iii), under high stringency conditions.~~

128. (Withdrawn-currently amended) A polynucleotide which is:

i) a catalytic polynucleotide capable of cleaving a polynucleotide whose sequence is ~~at least 95%~~ identical to the nucleotide sequence set forth in SEQ ID NO: 38, or

ii) a dsRNA molecule comprising a polynucleotide which is double-stranded over at least 19 basepairs whose sequence corresponds to a consecutive sequence set forth in SEQ ID NO: 38, or to a consecutive sequence which is ~~at least 95%~~ identical to the

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sequence set forth in SEQ ID NO: 38.

129. (Previously presented) A vector comprising or encoding the polynucleotide of claim 127.
130. (Withdrawn) A vector comprising or encoding the polynucleotide of claim 128.
131. (Currently amended) A—host plant or bacterial cell comprising the vector of claim 129.
132. (Withdrawn) A host cell comprising the vector of claim 130.
133. (Previously presented) A transgenic plant, the plant having been transformed with the polynucleotide of claim 127.
134. (Withdrawn) A transgenic plant, the plant having been transformed with the polynucleotide of claim 128.
135. (Currently amended) The transgenic plant of claim 133, which when compared to an isogenic non-transgenic plant, produces a modified level of a polypeptide comprising consecutive amino acids whose sequence is ~~at least 95%~~ identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38.
136. (Previously presented) The transgenic plant of claim 135, wherein the polypeptide comprises consecutive amino acids whose amino acid sequence is set forth in SEQ ID NO:12.

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137. (Currently amended) [[The]] A transgenic seed of the plant of claim 133.

138. (Withdrawn-currently amended) [[The]] A transgenic seed of the plant of claim 134.

139. (Previously presented) A process for producing fibre comprising obtaining the transgenic plant of claim 133 so as to thereby produce the fibre.

140. (Withdrawn-currently amended) A process of breeding a fibre producing plant having a polypeptide comprising consecutive amino acids whose sequence is ~~at least 95%~~ identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38, the process comprising analyzing the plant for a genetic variation in a polynucleotide whose sequence is ~~at least 95%~~ identical to the nucleotide sequence set forth in SEQ ID NO: 38, and/or analyzing the plant for a genetic variation in a polypeptide which is ~~at least 95%~~ identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38, and breeding the fibre producing plant.

141. (Withdrawn-currently amended) A process of selecting from a breeding population a fibre producing plant with altered fibre initiation and/or elongation potential, the method comprising:

- i) crossing two plants which have differing potential to produce fibre so as to produce

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progeny plants,

- ii) performing on the progeny plants a process comprising analyzing the plant for a genetic variation in a polynucleotide whose sequence is ~~at least 95%~~ identical to the nucleotide sequence set forth in SEQ ID NO: 38, and/or analyzing the plant for a genetic variation in a polypeptide whose amino acid sequence ~~which~~ is ~~at least 95%~~ identical to the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO: 38, and
- iii) selecting a progeny plant with altered fibre initiation and/or elongation potential when compared to a parent plant.

142. (Withdrawn-currently amended) A process for identifying an agent which reduces ~~alters~~ fibre initiation and/or elongation of a fibre producing plant, the method comprising:

- i) exposing a polynucleotide comprising consecutive nucleotides whose sequence is ~~at least 95%~~ identical to the nucleotide sequence set forth in SEQ ID NO: 38 to a candidate agent, and
- ii) assessing the ability of the candidate agent to hybridize and/or-cleave the polynucleotide.